CLAIM AMENDMENTS

1. *(Currently Amended)* A method of identifying a nucleic acid that encodes human telomerase reverse transcriptase (hTRT) or fragment thereof in a sample, comprising:

a) combining the sample with a polynucleotide probe such that the probe hybridizes specifically to the nucleic acid if the nucleic acid encodes ~~human telomerase reverse transcriptase (hTRT)~~ hTRT or fragment thereof;

b) detecting any hybrid formed as a result of a); and

c) identifying the nucleic acid as encoding hTRT or fragment thereof if the hybrid is detected;

wherein the probe hybridizes specifically to a DNA having the sequence of the hTRT encoding region of SEQ. ID NO:224 at 5°C to 25°C below T_m in aqueous solution at 1 M NaCl;

wherein T_m is the melting temperature of double-stranded DNA having the sequence of said encoding region under the same reaction conditions.

2. *(Currently Amended)* A method of detecting a nucleic acid that encodes hTRT or fragment thereof in a sample, comprising:

a) combining the sample with a polynucleotide probe such that the probe hybridizes specifically to a nucleic acid comprising at least 100 consecutive nucleotides contained in SEQ ID NO:224 if present in the sample; ~~and~~

b) detecting any hybrid formed as a result of a); and

c) identifying the nucleic acid as encoding hTRT or fragment thereof if the hybrid is detected;

wherein the polynucleotide probe consists essentially of a sequence identical or complementary to 25 or more consecutive nucleotides from the hTRT encoding region of SEQ ID NO:224.

3. *(Original)* The method of claim 2, wherein the hTRT nucleic acid is human genomic DNA.

4. *(Previously presented)* The method of claim 2, wherein the hTRT nucleic acid is mRNA or cDNA.

5. *(Currently Amended)* The method of claim 2, wherein the hTRT nucleic acid ~~comprises~~ consists essentially of 250 or more nucleotides of SEQ ID NO:224.

6. *(Currently Amended)* The method of claim 2, wherein the hTRT nucleic acid ~~comprises~~ consists essentially of 500 or more nucleotides of SEQ ID NO:224.

7. *(Currently Amended)* The method of claim 2, wherein the probe ~~comprises~~ consists essentially of a sequence identical or complementary to 30 or more consecutive nucleotides from the hTRT encoding region of SEQ ID NO:224.

8. *(Currently Amended)* The method of claim 2, wherein the probe ~~comprises~~ consists essentially of a sequence identical or complementary to 50 or more consecutive nucleotides from the hTRT encoding region of SEQ ID NO:224.

9. *(Currently Amended)* The method of claim 2, wherein the probe ~~comprises~~ consists essentially of a sequence identical or complementary to 100 or more consecutive nucleotides from the hTRT encoding region of SEQ ID NO:224.

10. *(Original)* The method of claim 2, wherein the probe comprises a sequence not contained in SEQ. ID NO:62.

11. *(Original)* The method of claim 9, wherein the probe comprises a sequence not contained in SEQ. ID NO:62.

12. *(Original)* The method of claim 2, wherein the sample is a human biological sample.

13. *(Currently Amended)* A method of identifying a nucleic acid that encodes hTRT or fragment thereof in a sample, comprising:

a) combining the sample with a polynucleotide primer under conditions that the primer specifically primes amplification of ~~the nucleic acid if the nucleic acid encodes human telomerase reverse transcriptase (hTRT)~~ SEQ. ID NO:224 or fragment thereof if present in the sample;

b) detecting any amplification product formed as a result of a); and

c) identifying the nucleic acid as encoding hTRT or fragment thereof if the amplification product is detected;

wherein the primer hybridizes specifically to a DNA having the sequence of the hTRT encoding region of SEQ. ID NO:224 at 5°C to 25°C below T_m in aqueous solution at 1 M NaCl;

wherein T_m is the melting temperature of double-stranded DNA having the sequence of said encoding region under the same reaction conditions.

14. *(Currently Amended)* A method of detecting a nucleic acid encoding hTRT or fragment thereof in a sample, comprising:

a) combining the sample with polynucleotide primers so as to prime amplification of nucleic acid encoding hTRT or fragment thereof if present in the sample; ~~and~~

b) detecting any amplified product formed as a result of a); and

c) identifying the nucleic acid as encoding hTRT or fragment thereof if the amplification product is detected;

wherein ~~the~~ each of said primers consists essentially of a sequence identical or complementary to 15 or more consecutive nucleotides from the hTRT encoding region of SEQ ID NO:224.

15. *(Previously presented)* The method of claim 14, wherein each of said primers consists essentially of a sequence identical or complementary to 30 or more consecutive nucleotides from the hTRT encoding region of SEQ ID NO:224.

16. *(Previously presented)* The method of claim 14, wherein each of said primers consists essentially of a sequence identical or complementary to 50 or more consecutive nucleotides from the hTRT encoding region of SEQ ID NO:224.

17. *(Original)* The method of claim 14, wherein the sample is a human biological sample.

18. *(Original)* The method of claim 14, wherein the sample comprises human genomic DNA.

19. *(Previously presented)* The method of claim 14, wherein the sample comprises hTRT mRNA or cDNA.

20. *CANCELLED.*

21. *(Original)* The method of claim 14, wherein the primers comprise a sequence not contained in SEQ. ID NO:62.

22. *CANCELLED*

23. *(Withdrawn)* A combination of oligonucleotide primers for PCR amplification for use in detecting an hTRT nucleic acid according to claim 14, wherein each primer consists essentially of a sequence identical or complementary to 15 or more consecutive nucleotides from the hTRT encoding region of SEQ ID NO:224.

24. *(Withdrawn)* The combination of primers of claim 23, wherein each primer consists of 15-30 nucleotides.

25. *(Withdrawn)* The combination of primers of claim 23, wherein each primer consists of 20-25 nucleotides.

26. *(Withdrawn)* The combination of primers of claim 23, wherein 50% or more of the nucleotides of each primer are guanine and/or cytosine.

27 to 34. *CANCELLED*

35. *(Previously presented)* The method of claim 1, wherein a) comprises combining the sample with the probe at 5°C to 25°C below T_m in aqueous solution at 1 M NaCl.

36. *(Previously presented)* The method of claim 1, wherein the hTRT nucleic acid is hTRT mRNA or cDNA.

37. *(Previously presented)* The method of claim 1, wherein the probe comprises a sequence identical or complementary to 100 or more consecutive nucleotides from the hTRT encoding region of SEQ ID NO:224.

38. *(Currently Amended)* The method of claim 1, wherein the ~~probe comprises a sequence~~ nucleic acid sequence of the probe is not contained in SEQ. ID NO:62.

39. *(Currently Amended)* The method of claim 1, wherein the sample has been taken from a patient ~~, and the method further comprises determining or assessing a tumor in the patient according to whether a nucleic acid encoding hTRT or an hTRT fragment is detected~~ having a tumor.

40. *(Currently Amended)* The method of claim 2, wherein the sample has been taken from a patient ~~, and the method further comprises determining or assessing a tumor in the patient according to whether a nucleic acid encoding hTRT or an hTRT fragment is detected~~ having a tumor.

41. *(Previously presented)* The method of claim 13, wherein a) comprises combining the sample with the primer at 5°C to 25°C below T_m in aqueous solution at 1 M NaCl.

42. *(Previously presented)* The method of claim 13, wherein the hTRT nucleic acid is mRNA or cDNA.

43. *(Previously presented)* The method of claim 13, wherein the primer comprises a sequence identical or complementary to 30 or more consecutive nucleotides from the hTRT encoding region of SEQ ID NO:224.

44. *(Previously presented)* The method of claim 13, wherein the primer comprises a sequence not contained in SEQ. ID NO:62.

45. *(Currently Amended)* The method of claim 13, wherein the sample has been taken from a patient ~~, and the method comprises determining or assessing a tumor in the patient according to whether a nucleic acid encoding hTRT or an hTRT fragment is detected~~ having a tumor.

46. *(Currently Amended)* The method of claim 14, wherein the sample has been taken from a patient ~~, and the method comprises determining or assessing a tumor in the patient according to whether said amplification product is formed~~ having a tumor.